

WHAT IS CLAIMED IS:

1. A recombinant nucleic acid molecule comprising a heterologous promoter sequence operably linked to a nucleic acid sequence, wherein the promoter sequence comprises a transcriptional regulatory region capable of mediating seed-specific expression in *Arabidopsis* wherein the transcriptional regulatory region:
- (a) is obtainable from a 5' region of a plant *FAE1* gene; or
- (b) hybridizes under stringent conditions to the 5' region of the plant *FAE1* gene; or
- (c) is at least 70% identical when optimally aligned to the 5' region of the plant *FAE1* gene.

2. The recombinant nucleic acid of claim 1 wherein the 5' region of the plant *FAE1* gene comprises (5' to 3'):

```

          AGA   TCTAAGAACA   CACATTCCCT   CAAATTTTAA   TGCACATGTA
ATCATAGTTT   AGCACAATTC   AAAAATAATG   TAGTATTAAA   GACAGAAATT
TGTAGACTTT   TTTTGGCGT   TAAAGGAAGA   CTAAGTTTAT   ACGTACATTT
TATTTTAAGT   GGAAAACCGA   AATTTTCCAT   CGAAATATAT   GAATTTAGTA
TATATATTTT   TGCAATGTAC   TATTTTGCTA   TTTTGGCAAC   TTTCAGTGGA
CTACTACTTT   ATTACAATGT   STATGGATGC   ATGAGTTTGA   GTATACACAT
GTCTAAATGC   ATGCTTTGCA   AAACGTAACG   GACCACAAAA   GAGGATCCAT
GCAAATACAT   CTCATAGCTT   CCTCCATTAT   TTTCCSACAC   AAACAGAGCA.

```

3. The recombinant nucleic acid of claim 1 wherein the 5' region of the plant *FAE1* gene comprises (5' to 3'):

```

AAGGCTTACC   CTATTAGTTG   AAAGTTGAAA   CTTTSTTCCC   TACTCAATTC
CTAGTTGTGT   AAATGTATGT   ATATGTAATG   CSTATAAAAC   CTAGTACTTA
AATGACTAGG   AGTGCTTCTT   GAGACCGATG   AGAGATGGGA   GCAGAACTAA
AGATCATGAC   ATAATTAAGA   ACGAATTTGA   AAGGCTCTTA   GTTTTCAATC
CTATTGAGAG   ATGTTTTTGT   CAAAGATAST   GCGGATTTTG   AACCAAGAA
AACATTTAAA   AAATCAGTAT   CCGGTTACGT   TCATGCAAAAT   AGAAAGTGGT
CTAGGATCTG   ATTGTAATTT   TAGACTTAAA   GAGTCTCTTA   AGATTCAATC
CTGGCTGTGT   ACAAACTAC   AAATAATATA   TTTTAGACTA   TTTGGCCTTA
ACTAAACTTC   CACTCATTAT   TTAATGAGGT   TAGAGAAATG   ACTTGCGAAT

```

AAACACATTC CCGAGAAATA CTCATGATCC CATAATTAGT CAGAGGGTAT
 GCCAATCAGA TCTAAGAACA CACATTCCCT CAAATTTTAA TGCACATGTA
 ATCATAGTTT AGCACAATTC AAAAATAATG TAGTATTAAA GACAGAAATT
 TGTAGACTTT TTTTGGCGT TAAAGGAAGA CTAAGTTTAT ACGTACATTT
 5 TATTTTAAGT GGAAAACCGA AATTTTCCAT CGAAATATAT GAATTTAGTA
 TATATATTTG TGCAATGTAC TATTTTGCTA TTTTGGCAAC TTTCASTGGA
 CTACTACTTT ATTACAATGT GTATGGATGC ATGAGTTTGA GTATACACAT
 GTCTAAATGC ATGCTTTGCA AAACGTAAGG GACCACAAAA GAGGATCCAT
 GCAAAATACAT CTCATAGCTT CCTCCATTAT TTTCCGACAC AAACAGAGCA.

10

4. The recombinant nucleic acid of claim 1 wherein the 5' region of the plant *FAE1* gene comprises (5' to 3'):

CTGACTTC ACCAAAGAAA CAACTCGAGT CGTTATCCAT
 CTCCTCATAA CCATCGCTCC ACTCTTTGSC TTCACCGTTT TCGGTTCCGT
 15 TCTCTACATC GCAACCCGGG CCAAAACGGT TTACCTCGTT GAGTACTCAT
 GCTACCTTCC ACCAACGCAT TGTAGATCAA GTATCTCCAA GGTGATGGAT
 ATCTTTTATC AAGTAAGAAA AGCTGATCCT TCTCGGAACG GCACGTGCGA
 TGACTCGTCC TGGCTTGACT TCTTGAGGAA GATTCAAGAA CGTTCAGGTC
 TAGGCGATGA AACTCACGGG CCGGAGGGGC TGCTTCAGGT CCTCCCCGG
 20 AAGACTTTTG CGGCGGCGCG TGAAGAGAGG GAGCAAGTTA TCATTSGTGC
 GCTAGAAAAT CTATTCAAGA ACACCAACGT TAACCCTAAA GATATAGGTA
 TACTTGTGGT GAACTCAAGC ATSTTTAATC CAACTCCATC GCTCTCCGCG
 ATGGTGGTTA ACACCTTCOA SCTCCGAAGC AACGTAAGAA GCTTTAACCT
 TGGTGGCATG CATTGTAGTG CCGGCTTAT AGCCATTGAT CTAGCAAAGG
 25 ACTTGTGGA TGTCCATAAA AATAGSTATG CTCTTGTGGT GAGCAGAGAG
 AACATCACTT ATAACATTTA CGCTGCTGAT AATAGSTCCA TGATGTTTTG
 AAATTGCTTG TTCCGTGTTG GTGGGGCCGC TATTTTGCTC TCCAACAAGC
 CTGGAGATCG TAGACGGTCC AAGTAGGAGC TAGTTCACAC GBTTCGAACG
 CATACCGGAG CTGACGACAA GTTTTTTGGT TGCTTGCAAC AAGGAGACGA
 30 TGAGAACGGG AAAATCGGAG TGAGTTTGTG CAAGGACATA ACCGATGTTG
 CTGGTGGAAC GGTAAAGAAA AACATAGCAA CGTTGGGTCC GTTGATTCTT
 CCGTTAAGCG AGAAACTTCT TTTTTTCTT ACCTTCATGG GCAAGAAACT
 TTTCAAGAT AAAATCAAA ATTACTAGCT CCGGATTTG AAACCTTGCTA
 TTGACCATTT TTGTATACAT GCGGAGGGA GAGCGGTGAT TGATGTGCTA
 35 GAGAAGAACC TAGCCCTAGC ACCGATCGAT GTAGAGGCAT CAAGATCAAC
 GTTACATAGA TTTGGAAACA GTTCATCTAG CTCAATATGG TATGAGTTGG

5
 10
 15
 20
 25
 30

CATACATAGA AGCAAAAGGA AGGATGAAGA AAGGTAAATA AGTTTGGCAG
 ATTGCTTTAG GGTGAGGCTT TAAGTGTAAC AGTGCAGTTT GGGTGGCTCT
 AAACAATGTC AAAGCTTCGA CAAATAGTCC TTGGGAACAC TGCATCGACA
 GATACCCGGT CAAAATTGAT TCTGATTGAG GTAAGTCAGA GACTCGTGTC
 CAAAACGGTC GGTCCTAATA AACGATGTTT GCTCTCTTTC GTTTCTTTTT
 ATTTGTTATA ATAATTTGAT GGCTACGATG TTTCTCTTGT TTGTTATGAA
 TAAAGAATGC AATGGTGTTT TAGTATTTGA TTGTTTTACA TGTATGATC
 TCTTATTTAC ATGAAATTTT TAAACGCCTA AAAAAAAAAA CGGAATTCCG.

- 10 5. The recombinant nucleic acid of claim 1 wherein the 5' region of the plant *F1E1* gene comprises (5' to 3'):

15
 20
 25
 30

CAGCTTAAC CGGTAAAATT
 GGCCTGTACA TATATTTACC ACTGAGTAAA GACATCAGTT AATGATTTGT
 TGTTACTCAA TTGGGCTAAG TGTATTATTA TATGTSTTGT ATATAATAAA
 GGTAGAACGT AAATTTACTA AGAATGTGTT TTTCCAATGT GATTGCTCTT
 TGGCCTCTTA GTTTTGAATC CTACTCGAGA AGACTAATTT TAATTTACTG
 GCAAAAATAG AAATCAATTT ATAAGTGTTT AAACAAATCG ATGGTATAAC
 TGATTAGTGA TCACTCTTAG GTTTTGATCC AACTCGAGTA TTCAGTATTG
 AACGCTTTTT TTAAATAAAA TCTTGATTTT TAAATTGGTT TTTTGAGTAA
 AAAAGTTCTT AATATTTTCT CTTTGTTTTA ATGGGTTTGT TTTGCATTTT
 ATAAGCTTAA TTTTCTAAT TTAATATTTT ATCTATCATC GTCCGTAAAG
 TTTTATTTGG CACAAACTTG TTTTACTTTT CTACCTTATA ATTTGGGAAC
 TGGTTGAGTC AAAGCGTACC GGACAAATAT GTTTTATATT CTTATTTAAG
 AATTAACACT CATCTCATTA TTAGTCAGAG GGTAGGGAGA TTCAGCCAAT
 CAATGCTAAC AACAAAATTC TCTTAATGAT CTAACGATGC TATTTAATAT
 TCGGATCAGT ATTCTTAAAT AAGAATATAA AACTAATTCA ATAGTTACAG
 ATAAAAACTT ATATAGACTT TTTTATTTGG AATATAAAAG TATCAATATA
 TTATAGACAA TATTTATAAC GTTAAAAATA CAATATTTAT ATTTTATATA
 TATTTATTTT AAATTGAAAA GCATTACTTC TATCGAAATG AATTTTAGTA
 TATTAATTAA TATTTTTTTA ATCGGACTAC TTTCTATTTT TGGCAGCTTT
 CATCTGACTA CTAATTTTAT TCAATGTGTA TGCATGCATG AGCATCAGTA
 ATACACATGT CTATATAAAT GCATGTAAAA CATAACGGAC CACAAAAGTG
 GATCCATAGA AATACATCTC ATCGGACCTT CTCCGACAGA AAATGAGACA.

6. The recombinant nucleic acid of claim 1 wherein the promoter sequence is selected from the group consisting of *Arabidopsis thaliana*, *Lunaria annua* and *Brassica napus* *FAE1* promoter sequences.

- 5 7. The recombinant nucleic acid of any one of claims 1 through 6, wherein the transcriptional regulatory region is at least 70% identical when optimally aligned to the 5' region of the plant *FAE1* gene.

8. The recombinant nucleic acid of claim 1 wherein the transcriptional regulatory region comprises (5' to 3'):

AGA TCTAAGAACA CACATTC CCT CAAATTTTAA TGCACATGTA
 ATCATAGTTT AGCACAATTC AAAAATAATG TAGTATTAAA GACAGAAATT
 TGTAGACTTT TTTTGGCGT TAAAGGAAGA CTAAGTTTAT ACGTACATTT
 TATTTTAAGT GGAAAACCGA AATTTTCCAT CGAAATATAT GAATTTAGTA
 15 TATATATTTT TGCAATGTAC TATTTTGCTA TTTTGGCAAC TTTCAGTGGA
 CTACTACTTT ATTACAATGT GTATGGATGC ATGAGTTTGA GTATACACAT
 GTCTAAATGC ATGCTTTGCA AACGTAACG GACCACAAAA GAGGATCCAT
 GCAAATACAT CTCATAGCTT CCTCCATTAT TTTCCGACAC AACAGAGCA.

20

9. The recombinant nucleic acid of claim 1 wherein the transcriptional regulatory region comprises (5' to 3'):

AAGGCTTACC CTATTAGTTG AAAGTTGAAA CTTTGTTCCT TACTCAATTC
 CTAGTTGTGT AAATGTATGT ATATGTAATG CCTATAAAAC CTAGTACTTA
 25 AATGACTAGG AGTGGTTCTT GAGACCGATG AGAGATGGGA GCAGAACTAA
 AGATGATGAC ATAATTAAGA ACGAATTTGA AAGGCTCTTA GGTTCGAATC
 CTATTCGAGA ATGTTTTTST CAAAGATAST GCGGATTTTG AACCAAAGAA
 AACATTTTAA AAATCAGTAT CCGGTTACGT TCATGCAAAAT AGAAAGTGGT
 CTAGGATCTG ATTGTAATTT TAGACTTAAA GAGTCTCTTA AGATTCAATC
 30 CTGGCTGTGT ACAAACACTAC AAATAATATA TTTTAGACTA TTTGGGCTTA
 ACTAAACTTC CACTCATTAT TTAATGAGST TAGAGAATAG ACTTGGCAAT
 AAACACATTC CCGAGAAATA CTCATGATCC CATAATTAGT CAGAGGGTAT
 GCCAATCAGA TCTAAGAACA CACATTC CCT CAAATTTTAA TGCACATGTA
 ATCATAGTTT AGCACAATTC AAAAATAATG TAGTATTAAA GACAGAAATT
 35 TGTAGACTTT TTTTGGCGT TAAAGGAAGA CTAAGTTTAT ACGTACATTT

TATTTTAAGT CGAAAACCGA AATTTTCCAT CGAAATATAT GAATTTAGTA
 TATATATTTT TGCAATGTAC TATTTTGCTA TTTTGGCAAC TTTTCAGTGA
 CTAATACTTT ATTACAATGT GTATGGATGC ATGAGTTTGA GTATACACAT
 GTCTAAATGC ATGCTTTTGA AAACGTAACG GACCACAAAA GAGGATCCAT
 5 GCAAATACAT CTCATAGCTT CCTCCATTAT TTTCCGACAC AAACAGAGCA.

10. The recombinant nucleic acid of claim 1 wherein the transcriptional regulatory region comprises (5' to 3'):

10

15

20

25

30

35

CTGACTTC ACCAAAGAAA CAACTCGAGT CGTTATCCAT
 CTCCTCATAA CCATCGCTCC ACTCTTTGCC TTCACCGTTT TCGGTTCCGGT
 TCTCTACATC GCAACCCGGC CCAAACCGGT TTACCTCGTT GAGTACTCAT
 GCTACCTTCC ACCAACGCAT TGTAGATCAA GTATCTCCAA GGTATGGAT
 ATCTTTTATC AAGTAAGAAA AGCTGATCCT TCTCGGAACG GCACGTGCGA
 TGACTCGTCG TGGCTTGACT TCTTGAGGAA GATTCAAGAA CGTTCAGGTC
 TAGGCGATGA AACTCACGGG CCGGAGGGGC TGCTTCAGGT CCGTCCCCGG
 AAGACTTTTG CGGCGGCGCG TGAAGAGACG GAGCAAGTTA TCATTGGTGC
 GCTAGAAAAT CTATTCAAGA ACACCAACGT TAACCTAAA GATATAGGTA
 TACTTGTGGT GAACTCAAGC ATGTTTAATC CAACTCCATC GCTCTCCGCG
 ATGGTCGTTA AACTTTTCAA GCTCCGAAGC AACGTAAGAA GCTTTAACCT
 TGGTGGCATG GGTGTAGTGC CCGGCGTTAT AGCCATTGAT CTAGCAAAGG
 ACTTGTTCGA TGTCCATAAA AATACGTATG CTCTTGTGGT GAGCACAGAG
 AACATCACTT ATAACATTTA CGCTGCTGAT AATAGCTCCA TCATGCTTTC
 AAATTGCTTC TCCGCTGCTC GTGGGGCCCC TATTTTCTTC TCCAAACAGC
 CTGGAGATCC TAGACGCTCC AAGTACGAGC TAGTTCCACAC GGTTCGAAGC
 CATACCGGAG CTGACGACAA GTCTTTTCGT TCCGTSCAAC AAGGAGACGA
 TGAGAACGGC AAAATCGGAG TSAGTTTGTC CAAGGACATA ACCGATGTTG
 CTGGTCGAAC GGTTAAGAAA AACATAGCAA CGTTGGGTCC GTTGATTCTT
 CCSTTAAGCG AGAAACTTCT TTTTTCCTT ACCTTCATGG GCAAGAAACT
 TTTCAAAGAT AAAATCAAC ATTACTACGT CCGGATTTT AAACCTTCCTA
 TTGACCATTG TTGTATACAT CCGGAGGCA GAGCCCTGAT TCATGTGCTA
 GAGAAGAACG TAGCCCTAGC ACCGATCGAT CTAGAGGCAT CAAGATCAAC
 GTTACATAGA TTTGGAACA GTTCATCTAG CTCATATATG TATGAGTTGG
 CATACATAGA AGCAAAAGGA AGGATGAAGA AAGGTAATAA AGTTTGGCAG
 ATTGCTTTAG GGTGAGGCTT TAAGTCTAAC AGTGCAGTTT GGGTSSCTCT
 AAACAATGTC AAAGCTTCGA CAAATAGTCC TTGGGAACAC TGCATCGACA

GATACCCGGT CAAAATTGAT TGTGATTCAG GTAAGTCAGA GACTCGTGTG
 CAAAACGGTC GGTCCTAATA AACGATGTTT GGTCTCTTTT GTTCTTTTTT
 ATTTGTTATA ATAATTTGAT GGCTACGATG TTTCTCTTGT TTGTTATGAA
 TAAAGAATGC AATGGTGTTC TAGTATTTGA TTGTTTTACA TGTATGTATC
 5 TGTATTTTAC ATGAAATTTT TAAACGCCTA AAAAAAAAAA CGGAATTCGG.

11. The recombinant nucleic acid of claim 1 wherein the transcriptional regulatory region comprises (5' to 3'):

10

CAGCTTAAC CGGTAAAATT
 GGCCTGTACA TATATTTACC ACTGAGTAAA GACATCAGTT AATGATTTGT
 TGTACTCAA TTGGGCTAAG TGTATTATTA TATGTGTTGT ATATAATPAA
 GGTAGAACGT AAATTTACTA AGAATGTGTT TTTCCAATGT GATTGCTCTT
 15 TGGCCTCTTA GGTTCGAATC CTACTCGAGA AGACTAATTT TAATTTACTG
 GCAAAAATAG AAATCAATTT ATAAGTGTTC AACCAATCG ATGGTATAAC
 TGATTAGTGA TCACTCTTAG GTTTTGATCC AACTCGAGTA TTGAGTATTG
 AACGCTTTTT TTAAATAAAA TCTTGATTTT TAAATTGGTT TTTTGAGTAA
 AAAAGTTCTT AATATTTTCT CTTTGTTTTA ATGGGTTTGT TTTGCATTTT
 20 ATAAGCTTAA TTTTCTAAT TTAATATTTT ATCTATCATC GTCCGTAAAG
 TTTTATTTGG CACAAACTTG TTTTACTTTT CTACCTTATA ATTTGGGAAC
 TGGTTGAGTC AAAGCGTACC GGACAATAT GTTTTATATT CTTATTTAAG
 AATTAACACT CATCTCATAA TTAGTCAGAG GCTAGGGAGA TTCAGCCAAT
 CAATGCTAAC AACAAAATTC TCTTAATGAT CTAACGATGC TATTTAATAT
 25 TCGGATCAAT ATTCTTAAT AGAATATAA ACTAATTC AATAGTTACAG
 ATAAAAACTT ATATAGACTT TTTTATTTGG AATATAAAG TATCAATATA
 TTATAGACAA TATTTATAAC GTTAAAAATA CAATATTTAT ATTTTATATA
 TATTTATTTG AAATTGAAAA GCATTACTTC TATCGAAATG AATTTTAGTA
 TATTAATTAA TATTTTTTTA ATCGGACTAC TTTCTATTTT TGGCACCTTT
 30 CATCTGACTA CTAATTTATT TCAATGTGTA TGCATGCATG AGCATSAGTA
 ATACACATGT CTAATATAAT GCATGTAAAA CTAACGGAC CACAAAAGTG
 GATCCATAGA AATACATCTC ATCGCACCTT CTCGGACACA AACTGAACA.

12. The recombinant nucleic acid of any one of claims 1 through 11 wherein the nucleic acid sequence encodes a translatable mRNA.

35

13. The recombinant nucleic acid of claim 12 wherein the nucleic acid sequence encodes an enzyme involved in lipid metabolism.
14. The recombinant nucleic acid of any one of claims 1 through 13, further comprising a transcription termination region operably linked to the nucleic acid sequence.
15. A host cell comprising the recombinant nucleic acid of any one of claims 1 through 14.
16. The host cell of claim 15, wherein the host cell is of a dicotyledonous plant species.
17. A plant comprising the recombinant nucleic acid of any one of claims 1 through 14.
18. The plant of claim 17, wherein the plant is of a dicotyledonous plant species.
19. A method of altering the phenotype of a seed comprising:
- a) transforming a seed-bearing plant, or a progenitor of the seed-bearing plant, with a vector comprising the nucleic acid of any one of claims 1 through 14;
 - b) growing the seed-bearing plant to obtain seed under conditions wherein the nucleic acid sequence is expressed during embryogenesis under the control of the transcriptional regulatory region to alter the phenotype of the seed.
20. A method of transforming a plant cell comprising transforming the plant cell with the recombinant nucleic acid of any one of claims 1 through 14.